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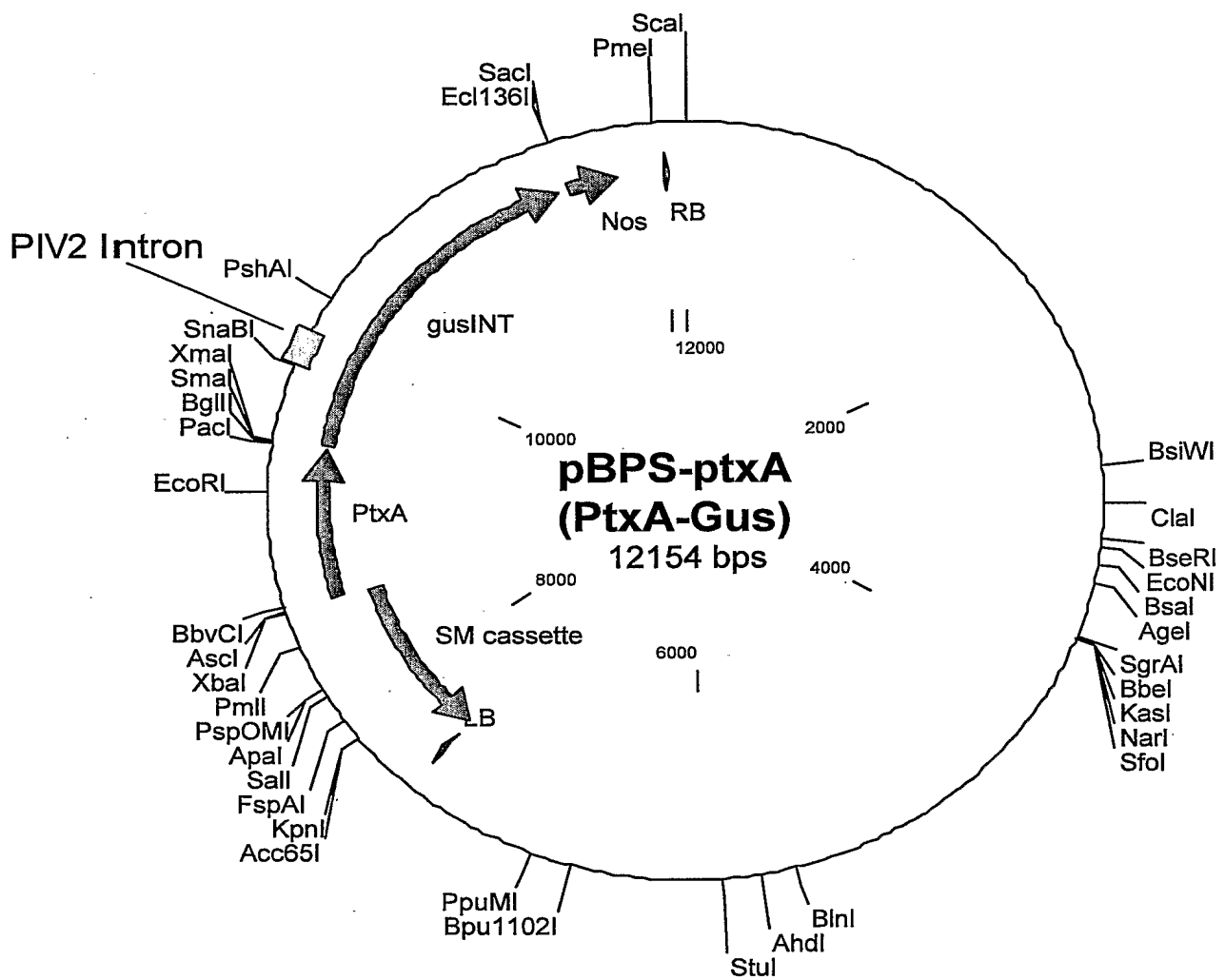


Fig. 1

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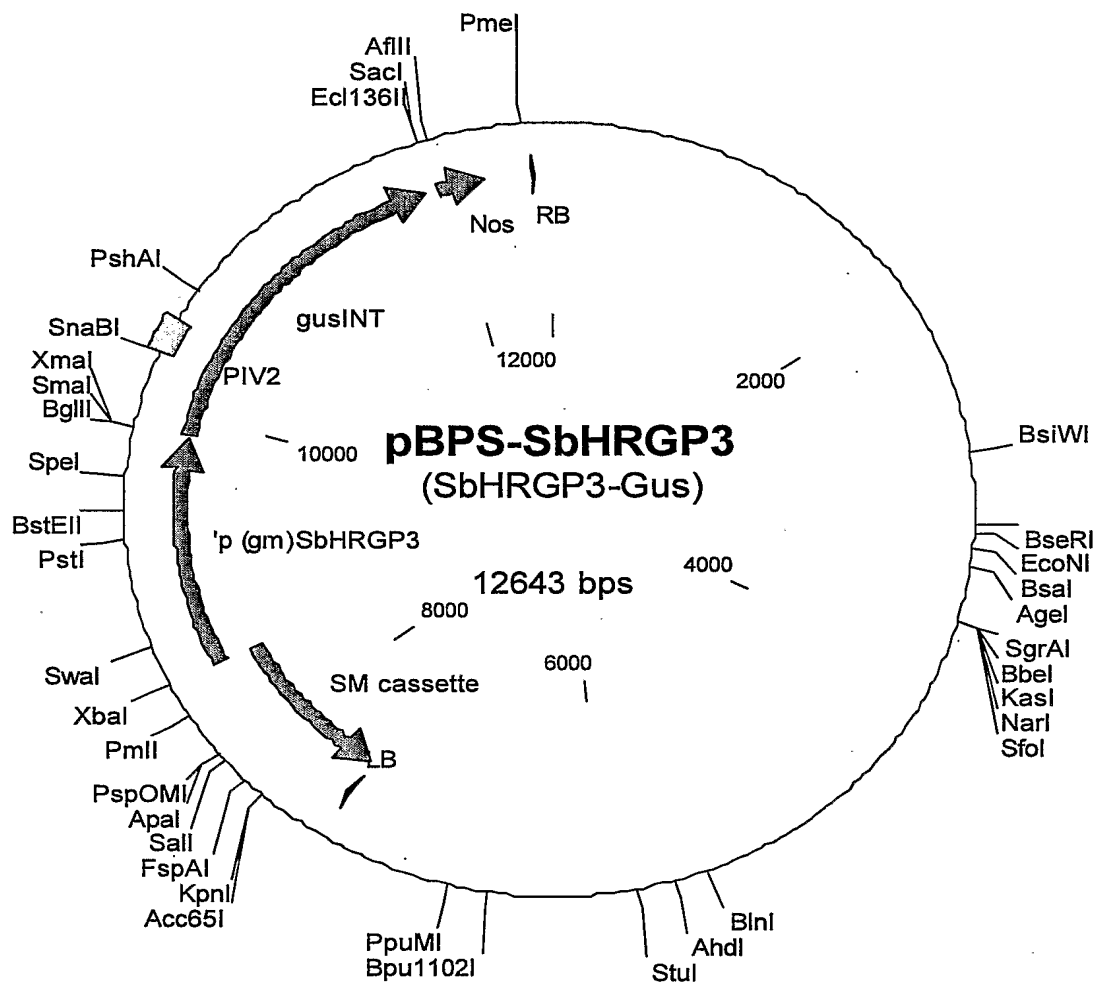
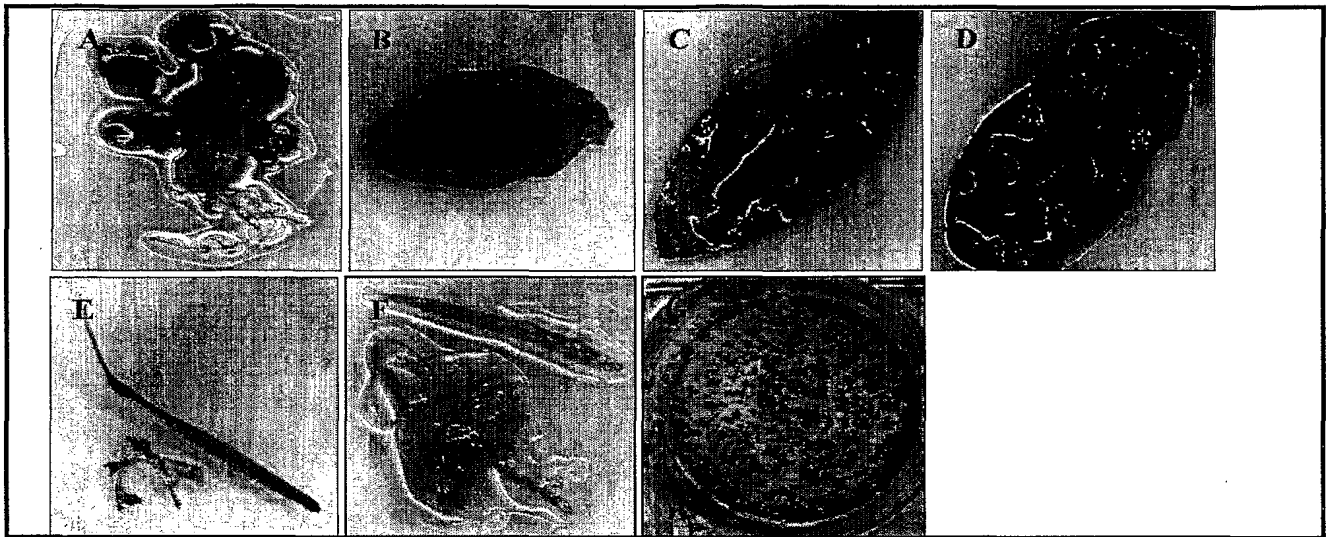


Fig. 2

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I



II

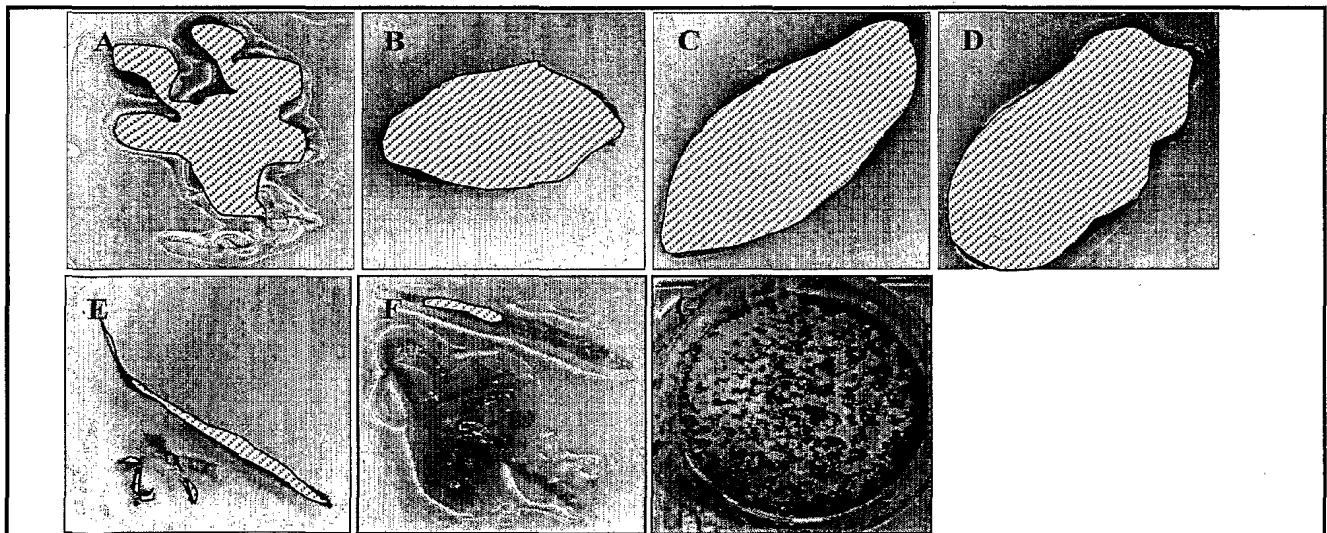
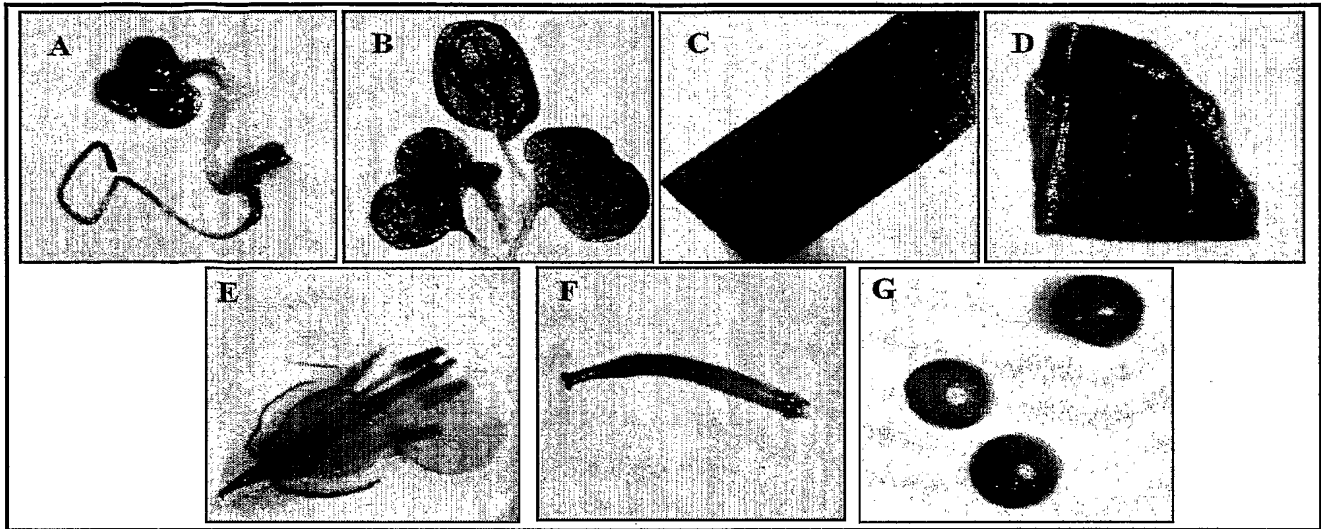


Fig 3

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I



II

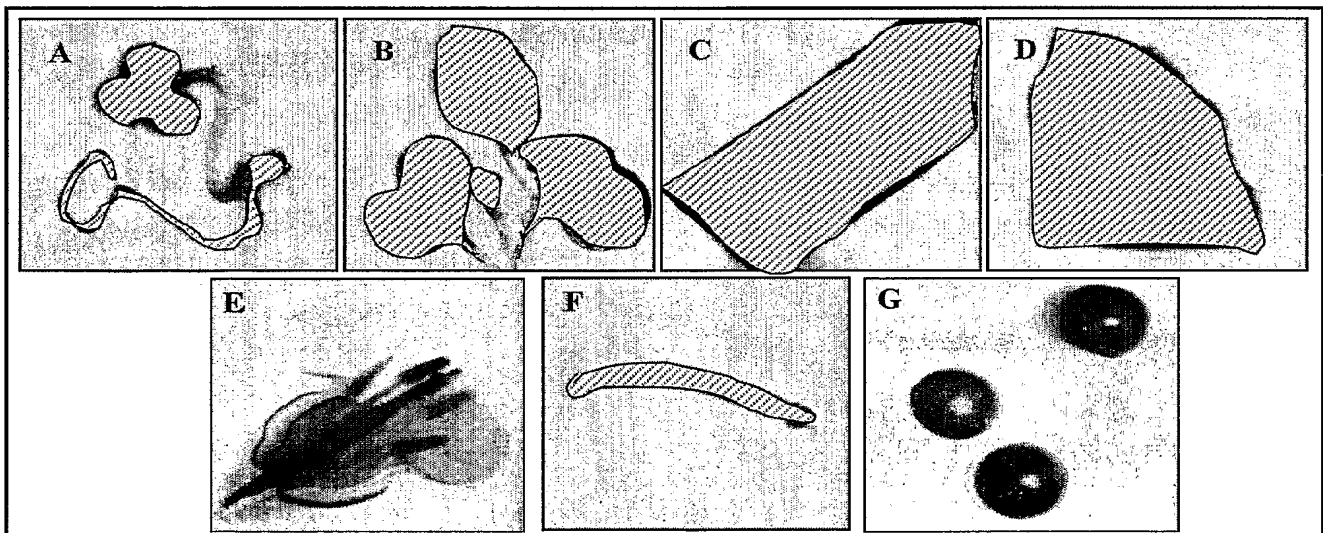


Fig 4

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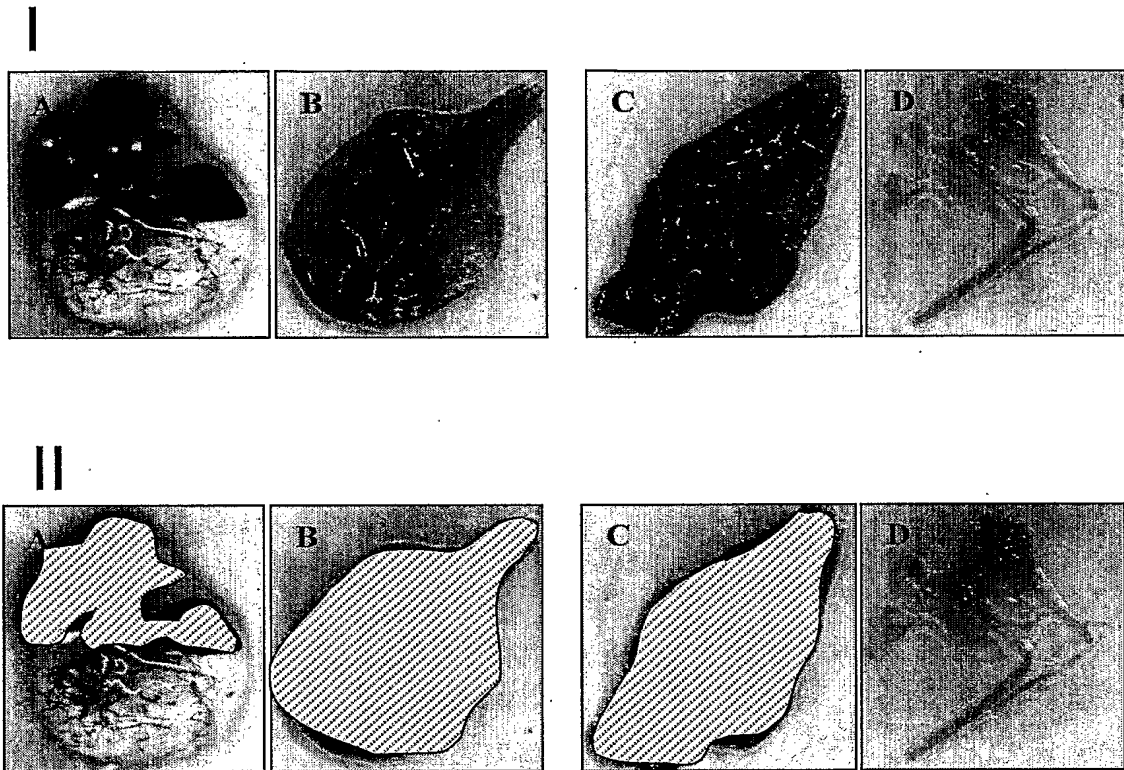


Fig 5

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| | | |
|-----------|--|-----|
| | 1 | 50 |
| A | (1) MANFAIANVLILLNLSTLLNLVACPYCPYPSPKPPTHKPPIVKPPVHK- | |
| B | (1) MANYALANVFILLNLSTLLNLVACPYCPYPSPKPPTHHPPIVKPPVHKR | |
| C | (1) ----- | |
| D | (1) -PHVKPPSTPKHPKDPPHVKPPSTPKQPPYVKPPTTPKHPPHVKPPS--- | |
| E | (1) MGKHGLATWLVILLNFATLLTSLACSYCPSPPSPP----- | |
| F | (1) MGSRLASEFVFLIFTVITLPPPTIQACTPCTRPHPPVVKP----- | |
| Consensus | (1) MA ALAS ILLN STLL LAC YCPYPSP PP PP VKPP | |
| | 51 | 100 |
| A | (50) -----PPKPQPCPPSSSPKPPHVKPPPHYKPPAVHP | |
| B | (51) RKYSPTPKPPVHKPPRYPPKPSPCPPSSSTPKPPHVKPPHHKPPVVHP | |
| C | (1) -----RAESART | |
| D | (47) -----TPKHHPKPP-----QKPCPPSSHGPKPPIVKP | |
| E | (35) -----KPP-----KVKHPLPPLPKHPPHVKP | |
| F | (41) -----PQHGGGGGGGSKPPPHGGGKGKPP | |
| Consensus | (51) PK PP K PH PPP H PKPP VKP | |
| | 101 | 150 |
| A | (83) PHVPKPP-AVHPPHVKPPVHPPIVHPPYVPK-----PPVVKPP----- | |
| B | (101) PHVPKPP-PVHPPYVPKPPIVKPPIVHPPYVPK-----PPVVKPPPYVPK | |
| C | (8) HHMFQP---HPP-YVPKPPIVKPPIVHPPYVPK-----PPVVKPP----- | |
| D | (75) PHVPRPP-IVHPPPIVSPSTPKPPKTPFTPKPPSPPIPIVSPP----- | |
| E | (57) PHTPMP-----PNPPAVKPPYVPK-----PPVVEPP----- | |
| F | (67) PHGGKGGGPPHHGGGGGGGKSPVVRPPPVVVRP---PPIIRPP----- | |
| Consensus | (101) PHVPKPP VHPYVPKPPIV PPIVHPPYVPK PPVVKPP | |
| | 151 | 200 |
| A | (122) --VVKPPHVKPPVVPVTPPYIPKPPIVFPPHVPLPP--VVPVTPPYVPK | |
| B | (144) PPVVRPPYVPKPPVVPVTPPYVPKPPVVRPPYVPKPP--VVPVTPPYVPK | |
| C | (44) -----PYVPKPPVVRPPYVPKPP--VVPVTPPYVLS | |
| D | (119) -----IVYPPITPTPIVHPPVTPKPPSPTPIIVSPPIVY | |
| E | (83) -----YVPKPPVVKPPYVPKPP--PVVEPPYMP | |
| F | (109) -----PVVYPPPIVRPPPIITRPPIIIPPIQPPPVTT | |
| Consensus | (151) V PPYVPKPPIVRPPYVPKPP VVPVTPPYVL | |
| | 201 | 250 |
| A | (168) P-----PIVFPPHVPLPPVVPVTPPYVP-----KPPIVFPPHVPLPPVVP | |
| B | (192) PPIVKPPIVFPPHVPLPPVVPSPPPYVSPPIVKPPIVFPPHVPLPPVVP | |
| C | (73) HHCFF-TTVSTSSCTITTTLCTNTPIVN-----HQLFFHHMFFYLPVVP | |
| D | (154) PPITPTPPVSPPIIPTPIIVSPFFVPN-----PPVV | |
| E | (108) ----- | |
| F | (140) PPGLLPPIITPPG--LLPPVTTPPGLLP-----PVTTPPG | |
| Consensus | (201) PP PIV PP V L P V SPPPIVP I F PL PVVP | |
| | 251 | 300 |
| A | (208) VTPPYVPLPPVVPVTPPFVPTPIIPTPTPTVPVSPSPSETPCPPPPPTV | |
| B | (242) VTPPYVQPP---PIVTPPTPTPIVTPPVSPPTP--PSETPCPPPLVP | |
| C | (116) VTPPYVQPT-----TYCNSTNTNTSNWTPPTP--PSETLVLPPLVP | |
| D | (186) IPPPYVPSPP-----PVVTPPIVTPPTPCPP-----PPPPPAI | |
| E | (108) -----H | |
| F | (173) LLPPIINPP-----PVTVPPPPSSGYPPYG-----PPSGG | |
| Consensus | (251) VTPPYVQPP P IV PP TPPTP PSET PPPP | |

Fig. 6a

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| | | |
|-----------|-------|--|
| | 301 | 350 |
| A | (258) | VPYPPPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD |
| B | (287) | YPPTPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD |
| C | (156) | YP-PPPAQQTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD |
| D | (219) | IP-SPPAQPTCPIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD |
| E | (109) | DT-----L---KLGACVDLLGGLVHIGIGSSAKDTCCPVLQGLVD |
| F | (202) | GGGGGGKQPTCPINALKLGACVDVLGGLIHIGLGNPVENVCCPVLQGLLE |
| Consensus | (301) | P PPAQPTCSIDALKLGACVDVLGGLIHIGIGGSAKQTCCPLLQGLVD |

| | | |
|-----------|-------|---|
| | 351 | 397 |
| A | (308) | LDAAVCLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPSS- |
| B | (337) | LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAY- |
| C | (205) | LDAAICLCTTIRLKLLNINLVIPLALQVLID-CGKTPPEGFKCPAS- |
| D | (268) | LDAAICLCTTIRLKLLNINIILPIALQVLIDDCGKYPPKDFKCPST- |
| E | (146) | LDAAVCLCTAIKVKLLNVNIIPIALQVLVG-CGKTTPPSGFQCPA-- |
| F | (252) | LEAAVCLCTTIRLKLLNLNIFIPLALQALIT-CGINPPSGFVCPPLT |
| Consensus | (351) | LDAAICLCTTIRLKLLNINIVIPALQVLID CGKTPPEGFKCPAS |

Fig. 6b

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551                                     600
B      (551) AAAAAC TAAAAAATAATTTCTCTCCTGATTTATATGAAATGACATTTTTTT
A      (1)  -----CGCAATTTTTTT
Consensus (551)                                     G  ATTTTTT

601                                     650
B      (601) TGGAACATGAAGG-GTATTGATTTTTTACCACCTTTTACACCT--TTCAAA
A      (12) GTGAAGCTGAGGGAGGATTGGATTTTACACCTATTCAAAAGTCATTCAAA
Consensus (601) GAA  TGA GG G ATTG  TTTTAC  C  TT A A  T  TTCAAA

651                                     700
B      (648) G-----CCATTCAAGGATGAATATAGATTTTTTGGGCGATCAAACAC
A      (62) GTTGTCCCTCCATTCAAGGATGAATGTAGATTTTTTCAAGCATCAAACAC
Consensus (651) G          CCATTCAAGGATGAAT  TAGATTTTT  ATCAAACAC

701                                     750
B      (689) AAGAATCATTACGATAACATGCTTTGGAACACACACATGCTTAAATTAAT
A      (112) AAGAATCACTAGCATAACATGCTTTGAAACCCACACA--CTTAAATTAAT
Consensus (701) AAGAATCA TA  ATAACATGCTTTG AAC CACACA  CTTAAATTAAT

751                                     800
B      (739) GGTGGAGTATCAAAT----TTTAAAT-ATTGTTGTCAAT-ACATACCC
A      (160) GTTAGGAATATCAAATCCAATATAAAATCATAGTTGTCAATTACATACTC
Consensus (751) G T GGA  TATCAAAT  T  TAAAT AT GTTGTCAAT ACATAC C

801                                     850
B      (783) CGTCAATCTTCTTTTTTTTACCCAATAAACATTGAAATGTTGCTTCTTTC
A      (210) AATCAAGTCCCTTTCTTTTACCCAATAAACATCAACATATGTCTTCTTC
Consensus (801) TCAA  CTTT TTTTACCCAATAAACAT  A AT TTGCTTCTT C

851                                     900
B      (833) GTTAAGCATAAAAAACATCAAAGTCTA-----GCAAAATGTTGTTTTTGC
A      (260) ATTAAGCATATAAACATCAAAGTCTAAACTAGCAAAATGTTGTTTTTAG
Consensus (851) TTAAGCATA AAACATCAAAGTCTA          GCAAAATGTTGTTTTT

901                                     950
B      (877) GATGACACATTTTCATA--TAGTTTAAAGGATGCATGATTGATTACAAAA
A      (310) GATGACACATTTTCATACATAGTTTAAAGATACTTGATTGATTACAAAA
Consensus (901) GATGACACATTTTCATA  TAGTTTAAA GAT C TGATTGATTACAAAA

951                                     1000
B      (925) AAAAAATACTAATAATTCTAGCACAAAGTTTAAAGCAAGATTATAAAGCT
A      (360) AGAAATTACCAATAGTT-TAGCACAAAGTCTAAAGCATAATTA--AAGCA
Consensus (951) A AAA  TAC AATA TT  TAGCACAAAGT TAAAGCA  ATTA  AAGC

1001                                     1050
B      (975) TCATAGCATGTGGATATTCATTTAGAAATATAGATTA-GATTGCCCTTT
A      (407) TCA---CATGTGCAGATTTAT---GAAAAAAGATTAAGATTGCCCTTT
Consensus (1001) TCA  CATGTG A ATT AT  GAAA A AGATTA GATTGCCCTTT

1051                                     1100
B      (1024) CATCACGGGTC---TAACAGCACCCTTGTCACCTACATGTCAAAA--TG
A      (451) CATCACGGGTCGAATAATAGCACTACTTGTCACCTACATGTAAAAAATG
Consensus (1051) CATCACGGGTC  TAA AGCAC ACTTGTCACCTACATGT AAAAA  TG

1101                                     1150
B      (1069) TCCTCTAGTACAGCACCGCTTTTTTACTTGATTCCCCTTGTCATGCATGA
A      (501) TCCTCTAGTACATCAAACCTTTTTCCATTGATTCCCCTTATCC----ATGA
Consensus (1101) TCCTCTAGTACA CA  TTTT  TTGATTCCCCTT TCC  ATGA

1151                                     1200
B      (1119) AAAAAATCAAAACAATATTTGGACACACAAACTTGCCCCACTTTCTTT
A      (547) AAAAAATAAACAATTCCTTAAGACACAAAAAATGGCCCCACAT-CCTTT
Consensus (1151) AAAAAAT AA A A T TT  GACACA AAA  TG CCCCAC T CCTTT

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Fig. 7a

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| | | | |
|-----------|--------|--|------|
| | 1201 | | 1250 |
| B | (1169) | TTCTTTCTGCCCTAGTTTGTGTTGAGACTCATATTGATCAAATTTGGCTAT | |
| A | (596) | ---TTTCTGGCCTAGTTTGTGTTGA----- | |
| Consensus | (1201) | TTTCTG CCTAGTTTGTGTTGA | |
| | 1251 | | 1300 |
| B | (1219) | GAATTCAAACAAAAAATTCACCTCTACCCATTGCATGTGT---GGGGCCCA | |
| A | (617) | -----A-----TTCATTCTAACTCTTGAATATGTAACGAGGCCCA | |
| Consensus | (1251) | A TTCA TCTA C TTG AT TGT G GGCCCA | |
| | 1301 | | 1350 |
| B | (1266) | CATATAAATCCATGAAGGATTTCAATGTCCATCCAAGTCAATGATTCAAC | |
| A | (652) | C-TAAAAATCAAT-----CAATGATTTAAC | |
| Consensus | (1301) | C TA AAATC AT CAATGATT AAC | |
| | 1351 | | 1400 |
| B | (1316) | ATATATAACATTGAATAATTTAATTCCAATTTGCAGTATTATGATTTAGA | |
| A | (676) | ATAAAAAA---TGAATAGTTTAATTCCAATTTGC----- | |
| Consensus | (1351) | ATA A AA TGAATA TTTAATTCCAATTTGC | |
| | 1401 | | 1450 |
| B | (1366) | TTGATTGCTGCAATACGGTCCGTGAATGTGATCACTCACGAGAAAGAGGT | |
| A | (707) | -----TGCAACATGGTCCGTGAATATGA---CTCACGAGAAAGATAT | |
| Consensus | (1401) | TGCAA A GGTCCGTGAAT TGA CTCACGAGAAAGA T | |
| | 1451 | | 1500 |
| B | (1416) | ATCAAAATTTCAAGGTATTTTATTTATTTTAAACAAATAAAATTTCAAGG | |
| A | (746) | ATCAAAATATCAA-----AATTTTCATAG | |
| Consensus | (1451) | ATCAAAAT TCAA AATTTCA G | |
| | 1501 | | 1550 |
| B | (1466) | TCTTGTTACCCATATAAACCTCCTCACTCACACCCAATTCTCTTAAGTGT | |
| A | (769) | TTTTTTTTCACCATATAAACCTCATCACTCATTC--TATTTTTTTTAAGTGC | |
| Consensus | (1501) | T TT TTCACCATATAAACCTC TCACTCA C ATT T TTAAGTG | |
| | 1551 | | 1600 |
| B | (1516) | ATGACTTCATAGTAC--ACTACACTACTTTCTTTGAAACATGGCTAACTA | |
| A | (817) | AAAGCTTCATAGTAGTGAGCACACACATTACACTAAAATCTTCGAAACTT | |
| Consensus | (1551) | A CTTTCATAGTA A ACAC TT C T AAA T AACT | |
| | 1601 | | 1650 |
| B | (1564) | TGCTCTAGCCAATGTTTTTCATCCTTCTCTTGAACCTTGAGTACCTTACTCA | |
| A | (867) | A----- | |
| Consensus | (1601) | | |

Fig. 7b

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| | | | |
|--------------|-------|--|-----|
| | 1 | | 50 |
| SEQ ID NO: 9 | (1) | ---CTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT | |
| SEQ ID NO: 8 | (1) | AAGCTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT | |
| SEQ ID NO: 7 | (1) | AAGCTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT | |
| Consensus | (1) | AAGCTTTTCAACAATCATGCCCATGTCAAGTGTA AACACAGGTTTACCTCT | |
| | 51 | | 100 |
| SEQ ID NO: 9 | (48) | CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA | |
| SEQ ID NO: 8 | (51) | CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA | |
| SEQ ID NO: 7 | (51) | CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA | |
| Consensus | (51) | CTTAAATAACCGTATTAAATGCTGAATGATGTATATATGTGGGTTCAAA | |
| | 101 | | 150 |
| SEQ ID NO: 9 | (98) | TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA | |
| SEQ ID NO: 8 | (101) | TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA | |
| SEQ ID NO: 7 | (101) | TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA | |
| Consensus | (101) | TTACATAAATTTGTAAGTATGTTACACATTGTATAAATATGTTTTAGAGAA | |
| | 151 | | 200 |
| SEQ ID NO: 9 | (148) | AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT | |
| SEQ ID NO: 8 | (151) | AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT | |
| SEQ ID NO: 7 | (151) | AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT | |
| Consensus | (151) | AAATGTAAACTTATATGTCTAAAGTTATAAAAGAAACATGTCCAACACAT | |
| | 201 | | 250 |
| SEQ ID NO: 9 | (198) | TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA | |
| SEQ ID NO: 8 | (201) | TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA | |
| SEQ ID NO: 7 | (201) | TTCAGTTAAGATTTAAATAGTATAA-TTAAAAATTATCGATGATGACAAA | |
| Consensus | (201) | TTCAGTTAAGATTTAAATAGTATAAATTAAAAATTATCGATGATGACAAA | |
| | 251 | | 300 |
| SEQ ID NO: 9 | (248) | AAATTGTAAATATAAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA | |
| SEQ ID NO: 8 | (251) | AAATTGTAAATATAAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA | |
| SEQ ID NO: 7 | (250) | AAATTGTAAATATAAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA | |
| Consensus | (251) | AAATTGTAAATATAAATTCATTTTAAAAAAAGTTAAGAAATTGAAAAAGGA | |
| | 301 | | 350 |
| SEQ ID NO: 9 | (298) | AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA | |
| SEQ ID NO: 8 | (301) | AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA | |
| SEQ ID NO: 7 | (300) | AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA | |
| Consensus | (301) | AATATCGAGAAAAAAATATGTCGATTATATATATGTGTGAGCTGAGTGAA | |
| | 351 | | 400 |
| SEQ ID NO: 9 | (348) | TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA | |
| SEQ ID NO: 8 | (351) | TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA | |
| SEQ ID NO: 7 | (350) | TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA | |
| Consensus | (351) | TATATATGTATATTTTATTTTGGACTGAATATATGTGTGTATAGACAATA | |
| | 401 | | 450 |
| SEQ ID NO: 9 | (398) | ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG | |
| SEQ ID NO: 8 | (401) | ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG | |
| SEQ ID NO: 7 | (400) | ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG | |
| Consensus | (401) | ATGCGCAGAATGCCGATCGATGAATTGTTTACTGCATTTCCAAATATGTG | |
| | 451 | | 500 |
| SEQ ID NO: 9 | (448) | TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG | |
| SEQ ID NO: 8 | (451) | TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG | |
| SEQ ID NO: 7 | (450) | TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG | |
| Consensus | (451) | TGCATAAGCGTTCCACATGTCACCCATGTTGTAATTAGTTTCTTCCCTGG | |
| | 501 | | 550 |

Fig. 8a

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SEQ ID NO: 9(498) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTTAAATTATGTA
SEQ ID NO: 8(501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTTAAATTATGTA
SEQ ID NO: 7(500) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTTAAATTATGTA
Consensus      (501) ATGAATTACTAAGAAACAGATTGATTGATAGTACTATATTTAAATTATGTA
                    551                                     600

SEQ ID NO: 9(548) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 8(551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
SEQ ID NO: 7(550) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
Consensus      (551) GCTTTACATGTCAGGAAAATGTAGTTGCAGTATTATGTAATGTAATTAAT
                    601                                     650

SEQ ID NO: 9(598) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 8(601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
SEQ ID NO: 7(600) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
Consensus      (601) AGGAAGTCACAGACAATTTGAAGACAATTTCTTTAGCTTACCTATCTCAT
                    651                                     700

SEQ ID NO: 9(648) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA-----
SEQ ID NO: 8(651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA-----
SEQ ID NO: 7(650) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAAAGCAAAA
Consensus      (651) GCCACAATTATGTACTTACGACAGTAAAATGTTTAAAAGCAAAA
                    701                                     750

SEQ ID NO: 9(692) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 8(695) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
SEQ ID NO: 7(700) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
Consensus      (701) AAAAGAAAGAAGAAGAAGAAGTAATAAATGGAATTATATAGAATGTACTC
                    751                                     800

SEQ ID NO: 9(742) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 8(745) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
SEQ ID NO: 7(750) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
Consensus      (751) TTTGTCTTCATCTGCCCTATAATTCCTGCAGCAGCCAAAGCATAATAGCA
                    801                                     850

SEQ ID NO: 9(792) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 8(795) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
SEQ ID NO: 7(800) TGCAATATGCACATATTCGTTTTAGGCTTTTAGC-TCCACGATCTGTTAA
Consensus      (801) TGCAATATGCACATATTCGTTTTAGGCTTTTAGCCTCCACGATCTGTTAA
                    851                                     900

SEQ ID NO: 9(842) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 8(845) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
SEQ ID NO: 7(849) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
Consensus      (851) TGGAAAGTGAAAAGTAAGAGATATGAAGTTCATTATGGCAGCCATGGTCC
                    901                                     950

SEQ ID NO: 9(892) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAAGGTCACCATGCATAA
SEQ ID NO: 8(895) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAAGGTCACCATGCATAA
SEQ ID NO: 7(899) CAGGGAAGCACTAGAAGATATGAAATGAC-TAAAAGGTCACCATGCATAA
Consensus      (901) CAGGGAAGCACTAGAAGATATGAAATGACATAAAAAGGTCACCATGCATAA
                    951                                     1000

SEQ ID NO: 9(942) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 8(945) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
SEQ ID NO: 7(948) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT
Consensus      (951) TGCTTTAAATGCTTGCTATAGAATCAAAAAATGAAGAGATGTGACAAATT

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Fig. 8b

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1001                                     1050
SEQ ID NO: 9(992) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 8(995) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
SEQ ID NO: 7(998) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
Consensus (1001) GTTACATCTAATACGCAATAATTTGACAAAGACGACTATGCGTTTATATA
1051                                     1100
SEQ ID NO: 9(1042) TTTATTTTAAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 8(1045) TTTATTTTAAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
SEQ ID NO: 7(1048) TTTATTTTAAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
Consensus (1051) TTTATTTTAAATTAGTTGGCGTCTCTTATTATAAAGAAAATAAGGGCAGTG
1101                                     1150
SEQ ID NO: 9(1092) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 8(1095) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
SEQ ID NO: 7(1098) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
Consensus (1101) TCAACATTTCCAGGCAACTAGTTAGTTATTTTATTTTCTTGTTTATAATT
1151                                     1200
SEQ ID NO: 9(1142) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
SEQ ID NO: 8(1145) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
SEQ ID NO: 7(1148) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
Consensus (1151) ATTTCCATATAGCTAGCTGTCTCTATCTAATCCAAATCCGCTTTCCACAA
1201                                     1250
SEQ ID NO: 9(1192) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 8(1195) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
SEQ ID NO: 7(1198) CCAACTTGGT-----CCAAAAAACTCAATATCAATATTTTCGAAAT
Consensus (1201) CCAACTTGGTCGCATTGGTCCAAAAAACTCAATATCAATATTTTCGAAAT
1251                                     1300
SEQ ID NO: 9(1242) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 8(1245) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
SEQ ID NO: 7(1239) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
Consensus (1251) AGTTTTAGCATTGTTTAGGAAGAGAATTGTAAGAGATAAAATCTAAGTAC
1301                                     1350
SEQ ID NO: 9(1292) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 8(1295) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
SEQ ID NO: 7(1289) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAA-GTTGTAT
Consensus (1301) TCCACCTACCAAGATAAAAATAGTTGGATAAAATGGGTAAAAAAAGTTGTAT
1351                                     1393
SEQ ID NO: 9(1342) AAAGGGCAACACTACCTCTCCTAATGGCAGTA-----
SEQ ID NO: 8(1345) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
SEQ ID NO: 7(1338) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG
Consensus (1351) AAAGGGCAACACTACCTCTCCTAATGGCAGTACCAAACCCAAG

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Fig. 8c

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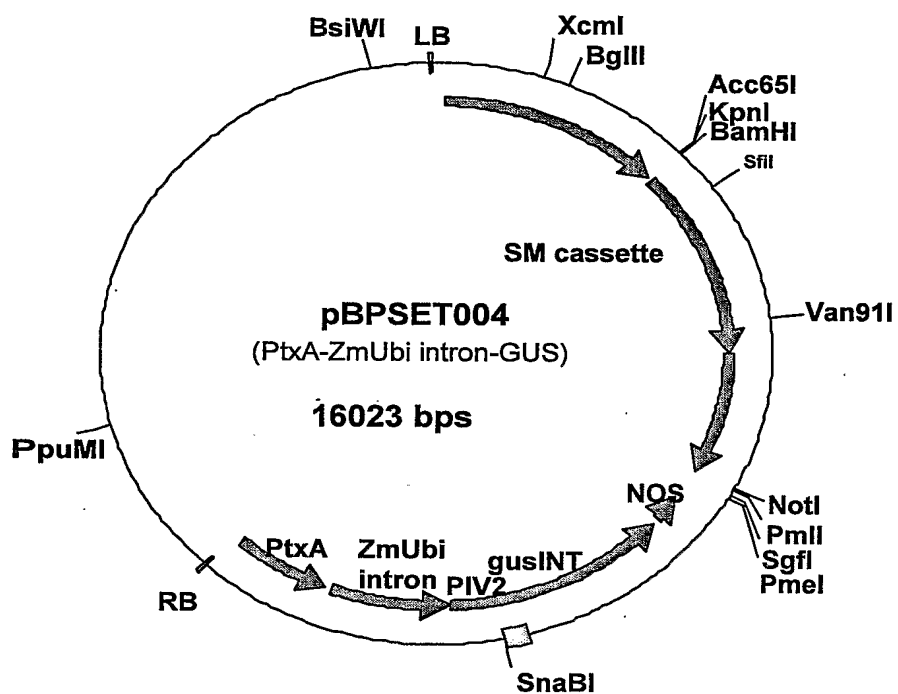


Fig. 9